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<120> APO-A-1 REGULATION OF T-CELL SIGNALING

<130> 06843.0035-00000

<140> 09/803,918

<141> 2001-03-13

<150> 60/189,008

<151> 2000-03-13

<150> 60/193,551

<151> 2000-03-31

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 801

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> (1)..(72)

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gtgtacgtgg	atgtgctcaa	agacagcggc	agagactatg	tgtcccagtt	tgaaggctcc	180
gccttgggaa	aacagctaaa	cctaaagctc	cttgacaact	gggacagcgt	gacctccacc	240
ttcagcaagc	tgcgcgaaca	gctcggccct	gtgaccagag	agttctggga	taacctggaa	300
aaggagacag	agggcctgag	gcaggagatg	agcaaggatc	tggaggaggt	gaaggccaag	360
gtgcagccct	acctggacga	cttccagaag	aagtggcagg	aggagatgga	gctctaccgc	420
cagaaggtgg	agccgctgag	cgcagagctc	caagagggag	cgcgccagaa	gctgcacgag	480
ctgcaagaga	agctgagccc	actgggagag	gagatgcgag	accgcgcgag	cgcccatgtg	540
gacgcgctgc	gcacgcatct	ggccccctac	agcgacgagc	tgcgccagcg	cttggccgag	600
cgccttgagg	ctctcaagga	gaacggcggc	gccagactgg	ccgagtacca	cgccaaggcc	660
accgagcatc	tgagcacgct	cagcgagaag	gccaaagccc	cgctcgagga	cctccgcca	720
ggcctgctgc	ccgtgctgga	gagcttcaag	gtcagcttcc	tgagcgctct	cgaggagtac	780
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<210> 2

<211> 267

<212> PRT

<213> Homo sapiens

<400> 2

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Gln	Ala	Arg	His	Phe	Trp	Gln	Gln	Asp	Glu	Pro	Pro	Gln	Ser	Pro	Trp
			20					25					30		

DAYER.APP

Asp Arg Val₃₅ Lys Asp Leu Ala Thr₄₀ Val Tyr Val₄₅ Asp Val Leu Lys Asp
 Ser Gly₅₀ Arg Asp Tyr Val₅₅ Ser Gln Phe Glu Gly₆₀ Ser Ala Leu Gly Lys
 Gln₆₅ Leu Asn Leu Lys₇₀ Leu Asp Asn Trp Asp₇₅ Ser Val Thr Ser Thr₈₀
 Phe Ser Lys Leu Arg₈₅ Glu Gln Leu Gly₉₀ Val Thr Gln Glu Phe₉₅ Trp
 Asp Asn Leu Glu₁₀₀ Lys Glu Thr Glu Gly₁₀₅ Leu Arg Gln Glu Met₁₁₀ Ser Lys
 Asp Leu Glu₁₁₅ Glu Val Lys Ala Lys₁₂₀ Val Gln Pro Tyr₁₂₅ Leu Asp Asp Phe
 Gln₁₃₀ Lys Lys Trp Gln Glu₁₃₅ Met Glu Leu Tyr Arg₁₄₀ Gln Lys Val Glu
 Pro₁₄₅ Leu Arg Ala Glu₁₅₀ Leu Gln Glu Gly Ala Arg₁₅₅ Gln Lys Leu His Glu₁₆₀
 Leu Gln Glu Lys₁₆₅ Leu Ser Pro Leu Gly₁₇₀ Glu Glu Met Arg Asp Arg₁₇₅ Ala
 Arg Ala His Val₁₈₀ Asp Ala Leu Arg Thr₁₈₅ His Leu Ala Pro Tyr₁₉₀ Ser Asp
 Glu Leu Arg₁₉₅ Gln Arg Leu Ala Ala₂₀₀ Arg Leu Glu Ala₂₀₅ Leu Lys Glu Asn
 Gly Gly₂₁₀ Ala Arg Leu Ala Glu₂₁₅ Tyr His Ala Lys Ala₂₂₀ Thr Glu His Leu
 Ser Thr Leu Ser Glu₂₃₀ Lys Ala Lys Pro Ala₂₃₅ Leu Glu Asp Leu Arg Gln₂₄₀
 Gly Leu Leu Pro Val₂₄₅ Leu Glu Ser Phe Lys₂₅₀ Val Ser Phe Leu Ser₂₅₅ Ala
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 <213> Homo sapiens

<220>
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 <222> (1)..(170)
 <223> 18 kDa N-terminal fragment

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DAYER.APP

Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp
 35 40 45
 Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu
 50 55 60
 Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu
 65 70 75 80
 Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys
 85 90 95
 Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met
 100 105 110
 Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu
 115 120 125
 Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu
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 Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg
 145 150 155 160
 Thr His Leu Ala Pro Tyr Ser Asp Glu Leu
 165 170

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 cagctaaacc taaagctcct tgacaactgg gacagcgtga cctccacctt cagcaagctg 180
 cgcgaacagc tcggccctgt gacccaggag ttctgggata acctggaaaa ggagacagag 240
 ggcctgaggc aggagatgag caaggatctg gaggaggtga aggccaaggt gcagccctac 300
 ctggacgact tccagaagaa gtggcaggag gagatggagc tctaccgcca gaaggtggag 360
 ccgctgcgcg cagagctcca agagggcgcg cgccagaagc tgcacgagct gcaagagaag 420
 ctgagcccac tgggcgagga gatgcgcgac cgcgcgcgcg cccatgtgga cgcgctgcgc 480
 acgcatctgg ccccctacag cgacgagctg 510